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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/977,034

DATE: 12/04/2001
TIME: 20:08:08

Input Set : N:\Crf3\RULE60\09977034.raw
Output Set: N:\CRF3\12042001\I977034.raw

1 <110> APPLICANT: Lo, Kin-Ming
2 Sun, Yaping
3 Gillies, Stephen D.
4 <120> TITLE OF INVENTION: Expression and Export of Interferon-Alpha Proteins as
5 Fc Fusion Proteins
6 <130> FILE REFERENCE: LEX-009
7 <140> CURRENT APPLICATION NUMBER: 09/977,034
8 <141> CURRENT FILING DATE: 2001-10-11
9 <150> PRIOR APPLICATION NUMBER: US/09/575,503
10 <151> PRIOR FILING DATE: 2000-05-19
11 <150> PRIOR APPLICATION NUMBER: US 60/134,895
12 <151> PRIOR FILING DATE: 1999-05-19
13 <160> NUMBER OF SEQ ID NOS: 29
14 <170> SOFTWARE: PatentIn Ver. 2.0
15 <210> SEQ ID NO: 1
16 <211> LENGTH: 498
17 <212> TYPE: DNA
18 <213> ORGANISM: Homo sapiens
19 <220> FEATURE:
20 <221> NAME/KEY: CDS
21 <222> LOCATION: (1)..(498)
22 <223> OTHER INFORMATION: Human IFN alpha DNA sequence
23 <400> SEQUENCE: 1
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27 1 5 10 15
28 ctc ctg gca caa atg gga aga atc tct cct ttc tcc tgc ctg aag gac 96
29 Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp
30 20 25 30
31 aga cat gac ttt gga ttc ccc cag gag ttt gat ggc aac cag ttc 144
32 Arg His Asp Phe Gly Phe Pro Gln Glu Phe Asp Gly Asn Gln Phe
33 35 40 45
34 cag aag gct caa gcc atc cct gtc ctc cat gag atg atc cag cag acc 192
35 Gln Lys Ala Gln Ala Ile Pro Val Leu His Glu Met Ile Gln Gln Thr
36 50 55 60
37 ttc aat ctc ttc agc aca aag gac tca tct gct act tgg gaa cag agc 240
38 Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Thr Trp Glu Gln Ser
39 65 70 75 80
40 ctc cta gaa aaa ttt tcc act gaa ctt aac cag cag ctg aat gac ctg 288
41 Leu Leu Glu Lys Phe Ser Thr Glu Leu Asn Gln Gln Leu Asn Asp Leu
42 85 90 95
43 gaa gcc tgc gtg ata cag gag gtt ggg gtg gaa gag act ccc ctg atg 336
44 Glu Ala Cys Val Ile Gln Glu Val Gly Val Glu Glu Thr Pro Leu Met
45 100 105 110
46 aat gtg gac tcc atc ctg gct gtg aag aaa tac ttc caa aga atc act 384
47 Asn Val Asp Ser Ile Leu Ala Val Lys Lys Tyr Phe Gln Arg Ile Thr
48 115 120 125

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49	ctt tat ctg aca gag aag aaa tac agc cct tgt gcc tgg gag gtt gtc	432
50	Leu Tyr Leu Thr Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val	
51	130 135 140	
52	aga gca gaa atc atg aga tcc ttc tct tta tca aaa att ttt caa gaa	480
53	Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Lys Ile Phe Gln Glu	
54	145 150 155 160	
55	aga tta agg aag aag gat	498
56	Arg Leu Arg Lys Lys Asp	
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61	<212> TYPE: PRT	
62	<213> ORGANISM: Homo sapiens	
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65	1 5 10 15	
66	Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp	
67	20 25 30	
68	Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe	
69	35 40 45	
70	Gln Lys Ala Gln Ala Ile Pro Val Leu His Glu Met Ile Gln Gln Thr	
71	50 55 60	
72	Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Thr Trp Glu Gln Ser	
73	65 70 75 80	
74	Leu Leu Glu Lys Phe Ser Thr Glu Leu Asn Gln Gln Leu Asn Asp Leu	
75	85 90 95	
76	Glu Ala Cys Val Ile Gln Glu Val Gly Val Glu Glu Thr Pro Leu Met	
77	100 105 110	
78	Asn Val Asp Ser Ile Leu Ala Val Lys Lys Tyr Phe Gln Arg Ile Thr	
79	115 120 125	
80	Leu Tyr Leu Thr Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val	
81	130 135 140	
82	Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Lys Ile Phe Gln Glu	
83	145 150 155 160	
84	Arg Leu Arg Lys Lys Asp	
85	165	
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88	<211> LENGTH: 696	
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94	<223> OTHER INFORMATION: Human Fc DNA sequence	
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97	Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala	
98	1 5 10 15	
99	cct gaa ctc ctg ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc	96

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102	aag	gac	acc	ctc	atg	atc	tcc	cgg	acc	cct	gag	gtc	aca	tgc	gtg	gtg	144					
103	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val						
104							35			40				45								
105	gtg	gac	gtg	agc	cac	gaa	gac	cct	gag	gtc	aag	ttc	aac	tgg	tac	gtg	192					
106	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val						
107							50			55				60								
108	gac	ggc	gtg	gag	gtg	cat	aat	gcc	aag	aca	aag	ccg	cg	gag	gag	cag	240					
109	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln						
110							65			70				75		80						
111	tac	aac	agc	acg	tac	cgt	gtg	gtc	agc	gtc	ctc	acc	gtc	ctg	cac	cag	288					
112	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln						
113							85			90				95								
114	gac	tgg	ctg	aat	ggc	aag	gag	tac	aag	tgc	aag	gtc	tcc	aac	aaa	gcc	336					
115	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala						
116							100			105				110								
117	ctc	cca	gcc	ccc	atc	gag	aaa	acc	atc	tcc	aaa	gcc	aaa	ggg	cag	ccc	384					
118	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro						
119							115			120				125								
120	cga	gaa	cca	cag	gtg	tac	acc	ctg	ccc	cca	tca	cg	gag	gag	atg	acc	432					
121	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Glu	Glu	Met	Thr						
122							130			135				140								
123	aag	aac	cag	gtc	agc	ctg	acc	tgc	ctg	gtc	aaa	ggc	ttc	tat	ccc	agc	480					
124	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser						
125							145			150				155		160						
126	gac	atc	gcc	gtg	gag	tgg	gag	agc	aat	ggg	cag	ccg	gag	aac	aac	tac	528					
127	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr						
128							165			170				175								
129	aag	acc	acg	ccc	gtg	ctg	gac	tcc	gac	ggc	tcc	ttc	ttc	ctc	tat		576					
130	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr						
131							180			185				190								
132	agc	aag	ctc	acc	gtg	gac	aag	agc	agg	tgg	cag	cag	ggg	aac	gtc	tcc	624					
133	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe						
134							195			200				205								
135	tca	tgc	tcc	gtg	atg	cat	gag	gct	ctg	cac	aac	cac	tac	acg	cag	aag	672					
136	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys						
137							210			215				220								
138	agc	ctc	tcc	ctg	tcc	ccg	ggt	aaa									696					
139	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys														
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149							Pro	Glu	Leu	Leu	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	

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150 20 25 30
 151 Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
 152 35 40 45
 153 Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
 154 50 55 60
 155 Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
 156 65 70 75 80
 157 Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
 158 85 90 95
 159 Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
 160 100 105 110
 161 Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
 162 115 120 125
 163 Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
 164 130 135 140
 165 Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
 166 145 150 155 160
 167 Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
 168 165 170 175
 169 Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
 170 180 185 190
 171 Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
 172 195 200 205
 173 Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
 174 210 215 220
 175 Ser Leu Ser Leu Ser Pro Gly Lys
 176 225 230
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 179 <211> LENGTH: 27
 180 <212> TYPE: DNA
 181 <213> ORGANISM: Homo sapiens
 182 <220> FEATURE:
 183 <223> OTHER INFORMATION: Forward PCR primer
 184 <400> SEQUENCE: 5
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 187 <210> SEQ ID NO: 6
 188 <211> LENGTH: 26
 189 <212> TYPE: DNA
 190 <213> ORGANISM: Homo sapiens
 191 <400> SEQUENCE: 6
 192 ctcgagtcaa tccttcctcc ttaatc 26
 194 <210> SEQ ID NO: 7
 195 <211> LENGTH: 162
 196 <212> TYPE: PRT
 197 <213> ORGANISM: Homo sapiens
 198 <220> FEATURE:
 199 <223> OTHER INFORMATION: IFN alpha consensus sequence wherein, Xaa at any
 200 position besides positions 24, 31, 70 and 129
 201 represents any amino acid.

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Input Set : N:\Crf3\RULE60\09977034.raw
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202 <223> OTHER INFORMATION: Xaa24 can be Ile or Leu, Xaa31 can be Lys or Gln,
203 Xaa70 can be Thr or Ser and Xaa 129 can be Leu or
204 Val.
205 <400> SEQUENCE: 7
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207 1 5 10 15
W--> 208 Xaa Xaa Xaa Xaa Met Xaa Xaa Xaa Ser Pro Xaa Xaa Cys Leu Xaa Xaa
209 20 25 30
W--> 210 Arg Xaa Asp Phe Xaa Xaa Pro Xaa Glu Xaa Xaa Xaa Xaa Xaa Gln Xaa
211 35 40 45
W--> 212 Xaa Xaa Xaa Gln Ala Xaa Xaa Val Leu Xaa Xaa Xaa Gln Gln Xaa
213 50 55 60
W--> 214 Xaa Xaa Leu Phe Xaa Xaa Xaa Xaa Ser Ala Xaa Trp Xaa Xaa Thr
215 65 70 75 80
W--> 216 Leu Leu Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Gln Gln Leu Xaa Asp Leu
217 85 90 95
W--> 218 Xaa Xaa Cys Xaa Leu Xaa
219 100 105 110
W--> 220 Xaa Val Xaa Xaa Xaa Leu Xaa Val Xaa Xaa Tyr Phe Xaa Xaa Ile Xaa
221 115 120 125
W--> 222 Xaa Tyr Leu Xaa Xaa Lys Xaa Xaa Ser Xaa Cys Ala Trp Glu Xaa Xaa
223 130 135 140
W--> 224 Xaa Xaa Xaa Xaa Met Arg Xaa Xaa Ser Xaa Xaa Xaa Xaa Leu Xaa Xaa
225 145 150 155 160
226 Arg Leu
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229 <211> LENGTH: 166
230 <212> TYPE: PRT
231 <213> ORGANISM: Homo sapiens
232 <220> FEATURE:
233 <223> OTHER INFORMATION: Human IFN alpha-1 protein
234 <400> SEQUENCE: 8
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237 Leu Leu Ala Gln Met Ser Arg Ile Ser Pro Ser Ser Cys Leu Met Asp
238 20 25 30
239 Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe
240 35 40 45
241 Gln Lys Ala Pro Ala Ile Ser Val Leu His Glu Leu Ile Gln Gln Ile
242 50 55 60
243 Phe Asn Leu Phe Thr Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Asp
244 65 70 75 80
245 Leu Leu Asp Lys Phe Cys Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu
246 85 90 95
247 Glu Ala Cys Val Met Gln Glu Glu Arg Val Gly Glu Thr Pro Leu Met
248 100 105 110
249 Asn Ala Asp Ser Ile Leu Ala Val Lys Lys Tyr Phe Arg Arg Ile Thr
250 115 120 125
251 Leu Tyr Leu Thr Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val

VERIFICATION SUMMARY
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Input Set : N:\Crf3\RULE60\09977034.raw
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L:208 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:7
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